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9/25/01
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/583,310

DATE: 09/25/2001
TIME: 09:31:48

Input Set : A:\16663-11.app
Output Set: N:\CRF3\09252001\I583310.raw

3 <110> APPLICANT: Cashman, John R.
4 Lomri, Nouredine
6 <120> TITLE OF INVENTION: DNA SEQUENCE ENCODING FLAVIN-CONTAINING MONOOXYGENASE
8 <130> FILE REFERENCE: 16663-1-2
10 <140> CURRENT APPLICATION NUMBER: 09/583,310
11 <141> CURRENT FILING DATE: 2000-05-30
13 <150> PRIOR APPLICATION NUMBER: 08/617,671
14 <151> PRIOR FILING DATE: 1996-03-27
16 <150> PRIOR APPLICATION NUMBER: 08/023,843
17 <151> PRIOR FILING DATE: 1993-02-26
19 <160> NUMBER OF SEQ ID NOS: 18
21 <170> SOFTWARE: PatentIn Ver. 2.1
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24 <211> LENGTH: 32
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA probe
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38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA probe
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49 <210> SEQ ID NO: 3
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51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence: AflIII site of
56 5' HLFMO-3 cDNA
58 <400> SEQUENCE: 3
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63 <211> LENGTH: 28
64 <212> TYPE: DNA
65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: Description of Artificial Sequence: Sal I site &
69 13 NT seq complementary to 3' end HLFMO-3 cDNA
71 <400> SEQUENCE: 4

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80 <220> FEATURE:
81 <221> NAME/KEY: CDS
82 <222> LOCATION: (1)..(1599)
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86 Met Gly Lys Lys Val Ala Ile Ile Gly Ala Gly Val Ser Gly Leu Ala
87 1 5 10 15
89 tcc atc agg agc tgt ctg gaa gag ggg ctg gag ccc acc tgc ttt gag 96
90 Ser Ile Arg Ser Cys Leu Glu Glu Gly Leu Glu Pro Thr Cys Phe Glu
91 20 25 30
93 aag agc aat gac att ggg ggc ctg tgg aaa ttt tca gac cat gca gag 144
94 Lys Ser Asn Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Ala Glu
95 35 40 45
97 gag ggc agg gct agc att tac aaa tca gtc ttt tcc aac tct tcc aaa 192
98 Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys
99 50 55 60
101 gag atg atg tgt ttc cca gac ttc cca ttt ccc gat gac ttc ccc aac 240
102 Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn
103 65 70 75 80
105 ttt atg cac aac agc aag atc cag gaa tat atc att gca ttt gcc aaa 288
106 Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys
107 85 90 95
109 gaa aag aac ctc ctg aag tac ata caa ttt aag aca ttt gta tcc agt 336
110 Glu Lys Asn Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser
111 100 105 110
113 gta aat aaa cat cct gat ttt gca act act ggc cag tgg gat gtt acc 384
114 Val Asn Lys His Pro Asp Phe Ala Thr Thr Gly Gln Trp Asp Val Thr
115 115 120 125
117 act gaa agg gat ggt aaa aaa gaa tcg gct gtc ttt gat gct gta atg 432
118 Thr Glu Arg Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met
119 130 135 140
121 gtt tgt tcc gga cat cat gtg tat ccc aac cta cca aaa aag tcc ttt 480
122 Val Cys Ser Gly His His Val Tyr Pro Asn Leu Pro Lys Lys Ser Phe
123 145 150 155 160
125 cca gga cta aac cac ttt aaa ggc aaa tgc ttc cac agc agg gac tat 528
126 Pro Gly Leu Asn His Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr
127 165 170 175
129 aaa gaa cca ggt gta ttc aat gga aag cgt gtc ctg gtg gtt ggc ctg 576
130 Lys Glu Pro Gly Val Phe Asn Gly Lys Arg Val Leu Val Val Gly Leu
131 180 185 190
133 ggg aat tcg ggc tgt gat att gcc aca gaa ctc agc cgc aca gca gaa 624
134 Gly Asn Ser Gly Cys Asp Ile Ala Thr Glu Leu Ser Arg Thr Ala Glu
135 195 200 205
137 cag gtc atg atc agt tcc aga agt ggc tcc tgg gtg atg agc cgg gtc 672

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138	Gln	Val	Met	Ile	Ser	Ser	Arg	Ser	Gly	Ser	Trp	Val	Met	Ser	Arg	Val	
139		210					215					220					
141	tgg	gac	aat	ggt	tat	cct	tgg	gac	atg	ctg	ctc	gtc	act	cga	ttt	gga	720
142	Trp	Asp	Asn	Gly	Tyr	Pro	Trp	Asp	Met	Leu	Leu	Val	Thr	Arg	Phe	Gly	
143	225					230					235					240	
145	acc	ttc	ctc	aag	aac	aat	tta	ccg	aca	gcc	atc	tct	gac	tgg	ttg	tac	768
146	Thr	Phe	Leu	Lys	Asn	Asn	Leu	Pro	Thr	Ala	Ile	Ser	Asp	Trp	Leu	Tyr	
147				245						250					255		
149	gtg	aag	cag	atg	aat	gca	aga	ttc	aag	cat	gaa	aac	tat	ggc	ttg	atg	816
150	Val	Lys	Gln	Met	Asn	Ala	Arg	Phe	Lys	His	Glu	Asn	Tyr	Gly	Leu	Met	
151				260						265					270		
153	cct	tta	aat	gga	gtc	ctg	agg	aaa	gag	cct	gta	ttt	aac	gat	gag	ctc	864
154	Pro	Leu	Asn	Gly	Val	Leu	Arg	Lys	Glu	Pro	Val	Phe	Asn	Asp	Glu	Leu	
155			275					280					285				
157	cca	gca	agc	att	ctg	tgt	ggc	att	gtg	tcc	gta	aag	cct	aac	gtg	aag	912
158	Pro	Ala	Ser	Ile	Leu	Cys	Gly	Ile	Val	Ser	Val	Lys	Pro	Asn	Val	Lys	
159		290					295					300					
161	gaa	ttc	aca	gag	acc	tcg	gcc	att	ttt	gag	gat	ggg	acc	ata	ttt	gag	960
162	Glu	Phe	Thr	Glu	Thr	Ser	Ala	Ile	Phe	Glu	Asp	Gly	Thr	Ile	Phe	Glu	
163	305					310					315					320	
165	ggc	att	gac	tgt	gta	atc	ttt	gca	aca	ggg	tat	agt	ttt	gcc	tac	ccc	1008
166	Gly	Ile	Asp	Cys	Val	Ile	Phe	Ala	Thr	Gly	Tyr	Ser	Phe	Ala	Tyr	Pro	
167				325						330					335		
169	ttc	ott	gat	gag	tct	atc	atc	aaa	agc	aga	aac	aat	gag	atc	att	tta	1056
170	Phe	Leu	Asp	Glu	Ser	Ile	Ile	Lys	Ser	Arg	Asn	Asn	Glu	Ile	Ile	Leu	
171				340						345					350		
173	ttt	aaa	gga	gta	ttt	cct	cct	cta	ctt	gag	aag	tca	acc	ata	gca	gtg	1104
174	Phe	Lys	Gly	Val	Phe	Pro	Pro	Leu	Glu	Lys	Ser	Thr	Ile	Ala	Val		
175			355					360					365				
177	att	ggc	ttt	gtc	cag	tcc	ott	ggg	gct	gcc	att	ccc	aca	ggt	gac	ctc	1152
178	Ile	Gly	Phe	Val	Gln	Ser	Leu	Gly	Ala	Ala	Ile	Pro	Thr	Val	Asp	Leu	
179		370					375					380					
181	cag	tcc	cgc	tgg	gca	gca	caa	gta	ata	aag	gga	act	tgt	act	ttg	cct	1200
182	Gln	Ser	Arg	Trp	Ala	Ala	Gln	Val	Ile	Lys	Gly	Thr	Cys	Thr	Leu	Pro	
183	385					390					395					400	
185	tct	atg	gaa	gac	atg	atg	aat	gat	att	aat	gag	aaa	atg	gag	aaa	aag	1248
186	Ser	Met	Glu	Asp	Met	Met	Asn	Asp	Ile	Asn	Glu	Lys	Met	Glu	Lys	Lys	
187				405						410					415		
189	cgc	aaa	tgg	ttt	ggc	aaa	agc	gag	acc	ata	cag	aca	gat	tac	att	gtt	1296
190	Arg	Lys	Trp	Phe	Gly	Lys	Ser	Glu	Thr	Ile	Gln	Thr	Asp	Tyr	Ile	Val	
191				420						425					430		
193	tat	atg	gat	gaa	ctc	tcc	tcc	ttc	att	ggg	gca	aag	ccc	aac	atc	cca	1344
194	Tyr	Met	Asp	Glu	Leu	Ser	Ser	Phe	Ile	Gly	Ala	Lys	Pro	Asn	Ile	Pro	
195			435					440					445				
197	tgg	ctg	ttt	ctc	aca	gat	ccc	aaa	ttg	gcc	atg	gaa	gtt	tat	ttt	ggc	1392
198	Trp	Leu	Phe	Leu	Thr	Asp	Pro	Lys	Leu	Ala	Met	Glu	Val	Tyr	Phe	Gly	
199		450					455					460					
201	cct	tgt	agt	ccc	tac	cag	ttt	agg	ctg	gtg	ggc	cca	ggg	cag	tgg	cca	1440
202	Pro	Cys	Ser	Pro	Tyr	Gln	Phe	Arg	Leu	Val	Gly	Pro	Gly	Gln	Trp	Pro	

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203 465          470          475          480
205 gga gcc aga aat gcc ata ctg acc cag tgg gac cgg tcg ttg aaa ccc 1488
206 Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp Arg Ser Leu Lys Pro
207          485          490          495
209 atg cag aca cga gtg gtc ggg aga ctt cag aag cct tgc ttc ttt ttc 1536
210 Met Gln Thr Arg Val Val Gly Arg Leu Gln Lys Pro Cys Phe Phe Phe
211          500          505          510
213 cat tgg ctg aag ctc ttt gca att cct att ctg tta atc gct gtt ttc 1584
214 His Trp Leu Lys Leu Phe Ala Ile Pro Ile Leu Leu Ile Ala Val Phe
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218 Leu Val Leu Thr
219          530
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223 <211> LENGTH: 532
224 <212> TYPE: PRT
225 <213> ORGANISM: Homo sapiens
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230 Ser Ile Arg Ser Cys Leu Glu Glu Gly Leu Glu Pro Thr Cys Phe Glu
231 20 25 30
232 Lys Ser Asn Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Ala Glu
233 35 40 45
234 Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys
235 50 55 60
236 Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn
237 65 70 75 80
238 Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys
239 85 90 95
240 Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser
241 100 105 110
242 Val Asn Lys His Pro Asp Phe Ala Thr Thr Gly Gln Trp Asp Val Thr
243 115 120 125
244 Thr Glu Arg Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met
245 130 135 140
246 Val Cys Ser Gly His His Val Tyr Pro Asn Leu Pro Lys Lys Ser Phe
247 145 150 155 160
248 Pro Gly Leu Asn His Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr
249 165 170 175
250 Lys Glu Pro Gly Val Phe Asn Gly Lys Arg Val Leu Val Val Gly Leu
251 180 185 190
252 Gly Asn Ser Gly Cys Asp Ile Ala Thr Glu Leu Ser Arg Thr Ala Glu
253 195 200 205
254 Gln Val Met Ile Ser Ser Arg Ser Gly Ser Trp Val Met Ser Arg Val
255 210 215 220
256 Trp Asp Asn Gly Tyr Pro Trp Asp Met Leu Leu Val Thr Arg Phe Gly
257 225 230 235 240
258 Thr Phe Leu Lys Asn Asn Leu Pro Thr Ala Ile Ser Asp Trp Leu Tyr

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259          245          250          255
260 Val Lys Gln Met Asn Ala Arg Phe Lys His Glu Asn Tyr Gly Leu Met
261          260          265          270
262 Pro Leu Asn Gly Val Leu Arg Lys Glu Pro Val Phe Asn Asp Glu Leu
263          275          280          285
264 Pro Ala Ser Ile Leu Cys Gly Ile Val Ser Val Lys Pro Asn Val Lys
265          290          295          300
266 Glu Phe Thr Glu Thr Ser Ala Ile Phe Glu Asp Gly Thr Ile Phe Glu
267 305          310          315          320
268 Gly Ile Asp Cys Val Ile Phe Ala Thr Gly Tyr Ser Phe Ala Tyr Pro
269          325          330          335
270 Phe Leu Asp Glu Ser Ile Ile Lys Ser Arg Asn Asn Glu Ile Ile Leu
271          340          345          350
272 Phe Lys Gly Val Phe Pro Pro Leu Leu Glu Lys Ser Thr Ile Ala Val
273          355          360          365
274 Ile Gly Phe Val Gln Ser Leu Gly Ala Ala Ile Pro Thr Val Asp Leu
275          370          375          380
276 Gln Ser Arg Trp Ala Ala Gln Val Ile Lys Gly Thr Cys Thr Leu Pro
277 385          390          395          400
278 Ser Met Glu Asp Met Met Asn Asp Ile Asn Glu Lys Met Glu Lys Lys
279          405          410          415
280 Arg Lys Trp Phe Gly Lys Ser Glu Thr Ile Gln Thr Asp Tyr Ile Val
281          420          425          430
282 Tyr Met Asp Glu Leu Ser Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro
283          435          440          445
284 Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Met Glu Val Tyr Phe Gly
285          450          455          460
286 Pro Cys Ser Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Gln Trp Pro
287 465          470          475          480
288 Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp Arg Ser Leu Lys Pro
289          485          490          495
290 Met Gln Thr Arg Val Val Gly Arg Leu Gln Lys Pro Cys Phe Phe Phe
291          500          505          510
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305 <221> NAME/KEY: CDS
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311 1 5 10 15
313 tcc atc agg agc tgt ctg gaa gag ggg ctg gag ccc acc tgc ttt gag 96

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VERIFICATION SUMMARY

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